

WEST Search History

Hide Items **Restore** **Clear** **Cancel**

DATE: Wednesday, March 21, 2007

Hide?	Set Name	Query	Hit Count
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L4	L3 and activity	229
<input type="checkbox"/>	L3	hepatoma derived growth factor	244
		<i>DB=USPT; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L2	L1 and hdgf	42
<input type="checkbox"/>	L1	hepatoma derived growth factor	49

END OF SEARCH HISTORY

d his

(FILE 'HOME' ENTERED AT 10:39:50 ON 21 MAR 2007)

FILE 'MEDLINE, EMBASE, BIOSIS' ENTERED AT 10:40:06 ON 21 MAR 2007

L1	173 S HDGF
L2	31 S L1 AND RAT
L3	17 DUPLICATE REMOVE L2 (14 DUPLICATES REMOVED)
L4	29052 S HRP
L5	197 S HEPATOMA DERIVED GROWTH FACTOR
L6	29 S L5 AND HUH-7
L7	11 DUPLICATE REMOVE L6 (18 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 10:42:33 ON 21 MAR 2007

FILE 'GENBANK' ENTERED AT 10:49:19 ON 21 MAR 2007

L8	1 S AY061636
L9	1 S BC085707
L10	1 S AF458587
L11	1 S AF458586

Day : Wednesday

Date: 3/21/2007

Time: 08:34:32

 PALM INTRANET

Inventor Information for 10/501053

Inventor Name	City	State/Country
<u>YU, LONG</u>	SHANGHAI	CHINA
<u>TANG, LISHA</u>	SHANGHAI	JAPAN
<u>GUO, ZEKUN</u>	SHANGHAI	CHINA
<u>ZHANG, PINGZHAO</u>	SHANGHAI	CHINA
<u>DONG, YIMIN</u>	SHANGHAI	CHINA

[Appln Info](#)[Contents](#)[Petition Info](#)[Atty/Agent Info](#)[Continuity/Reexam](#)[Foreign E](#)Search Another: Application# or Patent# PCT / / or PG PUBS # Attorney Docket # Bar Code #

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Day : Wednesday

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Continuity Information for 10/501053

Parent Data

10501053is a national stage entry of PCT/CN03/00003 International Filing Date: 01/02/2003

Child Data

No Child Data

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: November 22, 2006, 19:14:17 ; Search time 5625 Seconds
(without alignments)
11254.746 Million cell updates/sec

Title: US-10-501-053-1
Perfect score: 990
Sequence: 1 cgctatgtcttgcttcagcc.....ttgggaaaccgctagggcc 990

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	966	97.6	2068	6 BC085707	BC085707 Rattus no
2	966	97.6	338115	12 AC111953	AC111953 Rattus no
3	924.4	93.4	1512	6 AY061636	AY061636 Rattus no
4	907.4	91.7	909	5 AF458587	AF458587 Homo sapi
5	885.4	89.4	921	6 AF458586	AF458586 Rattus no
6	572.6	57.8	2046	6 BC108388	BC108388 Mus muscu

c	7	572.6	57.8	188325	6	AL662807	AL662807 Mouse DNA
c	8	572.6	57.8	204891	12	AL837519	AL837519 Mus muscu
	9	571	57.7	1332	2	E14400	E14400 cDNA encodi
	10	571	57.7	1333	6	D63663	D63663 Mus musculu
	11	511.8	51.7	870	5	AF451983	AF451983 Homo sapi
	12	503.6	50.9	1856	6	AF180109	AF180109 Mus muscu
	13	347.8	35.1	783	2	E17007	E17007 DNA encodin
	14	276.4	27.9	495	5	AF451984	AF451984 Homo sapi
c	15	237.2	24.0	110000	12	CT030694_3	Continuation (4 of
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	17	226.8	22.9	880	2	AR481891	AR481891 Sequence
	18	226.8	22.9	880	2	AX111704	AX111704 Sequence
	19	226.8	22.9	143429	5	HS309H15	AL033539 Human DNA
	20	222	22.4	2034	5	AK056824	AK056824 Homo sapi
	21	211.6	21.4	2147	14	BC109529	BC109529 Bos tauru
	22	211.6	21.4	188230	12	AC159382	AC159382 Bos tauru
	23	208.4	21.1	1942	14	BTA237666	AJ237666 Bos tauru
	24	179.4	18.1	180286	6	AL645600	AL645600 Mouse DNA
	25	177.8	18.0	124244	6	AL929026	AL929026 Mouse DNA
c	26	175.6	17.7	186202	6	AC125319	AC125319 Mus muscu
c	27	173.2	17.5	194303	6	AC154296	AC154296 Mus muscu
	28	170.8	17.3	152842	6	AC156500	AC156500 Mus muscu
	29	170	17.2	213866	6	AC114589	AC114589 Mus muscu
c	30	170	17.2	234919	6	AC121887	AC121887 Mus muscu
c	31	166.6	16.8	157754	6	AC132313	AC132313 Mus muscu
	32	166.6	16.8	228033	6	AC168050	AC168050 Mus muscu
c	33	166.4	16.8	175398	6	AC102151	AC102151 Mus muscu
c	34	165.8	16.7	144094	6	AC109193	AC109193 Mus muscu
c	35	165.4	16.7	200574	6	BX005304	BX005304 Mouse DNA
c	36	165.2	16.7	186404	6	AC169630	AC169630 Mus muscu
	37	165.2	16.7	205054	6	AC098712	AC098712 Mus muscu
	38	165	16.7	116887	6	AL929153	AL929153 Mouse DNA
c	39	165	16.7	181676	6	AC124194	AC124194 Mus muscu
c	40	165	16.7	200180	12	AC169629	AC169629 Mus muscu
c	41	164.6	16.6	174139	12	AC116700	AC116700 Mus muscu
	42	163.6	16.5	171554	6	AC142228	AC142228 Mus muscu
	43	163.6	16.5	183408	6	AC119873	AC119873 Mus muscu
	44	163	16.5	163916	6	AC141887	AC141887 Mus muscu
c	45	162.8	16.4	191753	6	AC125235	AC125235 Mus muscu

ALIGNMENTS

RESULT 1

BC085707

LOCUS BC085707 2068 bp mRNA linear ROD 20-OCT-2005

DEFINITION Rattus norvegicus hepatoma-derived growth factor, related protein 1, mRNA (cDNA clone MGC:93218 IMAGE:7132556), complete cds.

ACCESSION BC085707

VERSION BC085707.1 GI:55715911

KEYWORDS MGC.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 2068)

AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
 Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
 Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
 Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
 Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
 Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
 McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
 Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
 Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
 Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,
 Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
 Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
 Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
 Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

CONSRTM Mammalian Gene Collection Program Team
 TITLE Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 2068)
 AUTHORS .
 CONSRTM NIH MGC Project
 TITLE Direct Submission
 JOURNAL Submitted (01-NOV-2004) National Institutes of Health, Mammalian
 Gene Collection (MGC), Bethesda, MD 20892-2590, USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Howard Jacobs
 cDNA Library Preparation: Express Genomics
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 184 Row: p Column: 12
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 19424221.

FEATURES Location/Qualifiers
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 CDS 31. .945
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/db_xref="RGD:621012"
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AEVMAVVVEEPESLKRSAEDEQPHSPKPRPRAAPGALEMEPAGEREA EACFVFEEDQ
AOEOOTPLEEEATEEAVOGLMVGEIEGL"
```

ORIGIN

Query Match 97.6%; Score 966; DB 6; Length 2068;
Best Local Similarity 98.9%; Pred. No. 1.7e-223;
Matches 985; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

Qy	1	CGCTATGCTCTTGCTTCAGCCGCCCAAAATACAAGACCGGGGACCTGGTGTGTTTGCCAAATT	60
Db	27	CGCCATGTCTTGCTTCAGCCGCCCAAAATACAAGACCGGGGACCTGGTGTGTTTGCCAAATT	86
Qy	61	AAAGGGCTATGCCCATTGGCCAGCGAGGATTGAACATGTCACCTGAACCCAACCGCTACCA	120
Db	87	AAAGGGCTATGCCCATTGGCCAGCGAGGATTGAACATGTCACCTGAACCCAACCGCTACCA	146
Qy	121	GGTGTTCCTTCTTCGGGACCCATGAGACCGCCCTGCTGGGCCCAAGCACCTTTTTCCTTA	180
Db	147	GGTGTTCCTTCTTCGGGACCCATGAGACCGCCCTGCTGGGCCCAAGCACCTTTTTCCTTA	206
Qy	181	TGAGGAGTCCAAGGAGAGGTTCGGCAAGCCTAACAAGAGGCGCGGCTTCAGTGAGGGGCT	240
Db	207	TGAGGAGTCCAAGGAGAGGTTCGGCAAGCCTAACAAGAGGCGCGGCTTCAGTGAGGGGCT	266
Qy	241	GTGGGAGATCGAGCACGACCCTATGGCTGAGGCCTCCCCTGCCTGTGCCCAGATGAGGA	300
Db	267	GTGGGAGATCGAGCACGACCCTATGGTTGAGGCCTCCCCTGCCTGTGCCCAGATGAGGA	326
Qy	301	GCAGCTTTGTGCCGAGGAGCCAGGGCCAGGAGAGGAGCCAGAGCCGGGGCAGGAGCTGGA	360
Db	327	GCAGCTTTGTGCCGAGGAGCCAGGGCCAGGAGAGGAGCCAGAGCCGGGGCAGGAGCTGGA	386
Qy	361	GCCGGAATCCAGGCCTGAGCTGGAATCCATGCCTGAGCTGGAGGCAGAACCGAGGCCTGA	420
Db	387	GCCGGAATCCAGGCCTGAGCTGGAATCCATGCCTGAGCTGGAGGCAGAACCGAGGCCTGA	446
Qy	421	GAAAGAGTGTGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCTGGAGCAGGAGCCGGA	480
Db	447	GAAAGAGTGTGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCTGGA	506
Qy	481	GCTGGAGCC-----GGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCCGAGCCCGA	534
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Db      627 CATTGAGGCCGAGCCAGGAGATCAGCAAGCCGAGCAAGTGCAGAGAGCAGCACGCTGAAGC 686
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```

RESULT 2

AC111953

LOCUS AC111953 338115 bp DNA linear HTG 09-NOV-2002

DEFINITION Rattus norvegicus clone CH230-211F3, *** SEQUENCING IN PROGRESS
***, 6 unordered pieces.

ACCESSION AC111953

VERSION AC111953.4 GI:24818630

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 338115)

AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
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Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
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Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
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Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
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Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
 Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
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 Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
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 Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
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 Nwaokemeleh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
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 Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
 Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
 Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
 Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
 Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
 Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
 Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
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 Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
 Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
 Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
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 Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
 Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
 Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
 Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 338115)
 AUTHORS Worley,K.C.
 TITLE Direct Submission
 JOURNAL Submitted (19-FEB-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 REFERENCE 3 (bases 1 to 338115)
 AUTHORS Rat Genome Sequencing Consortium.
 TITLE Direct Submission
 JOURNAL Submitted (09-NOV-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 COMMENT On Nov 9, 2002 this sequence version replaced gi:23101342.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GOSJ

Center clone name: CH230-211F3

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 233778 bases at least Q40

Consensus quality: 236747 bases at least Q30

Consensus quality: 238950 bases at least Q20

Estimated insert size: 235437; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 6 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 12369: contig of 12369 bp in length
 * 12370 12469: gap of unknown length
 * 12470 34481: contig of 22012 bp in length
 * 34482 34581: gap of unknown length
 * 34582 329483: contig of 294902 bp in length
 * 329484 329583: gap of unknown length
 * 329584 330973: contig of 1390 bp in length
 * 330974 331073: gap of unknown length
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 * 334104 338115: contig of 4012 bp in length.

FEATURES	Location/Qualifiers
source	1. .338115 /organism="Rattus norvegicus" /mol_type="genomic DNA" /db_xref="taxon:10116" /clone="CH230-211F3"
gap	12370. .12469 /estimated_length=unknown
misc_feature	12470. .13894 /note="wgs_contig"
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misc_feature	56734. .58848 /note="wgs_contig"
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gap	329484. .329583 /estimated_length=unknown
gap	330974. .331073 /estimated_length=unknown
gap	334004. .334103 /estimated_length=unknown

ORIGIN

Query Match 97.6%; Score 966; DB 12; Length 338115;
 Best Local Similarity 98.9%; Pred. No. 1.9e-223;
 Matches 985; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

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Qy	61	AAAGGGCTATGCCATTGGCCAGCGAGGATTGAACATGTCACTGAACCCAACCGCTACCA	120
Db	117044	AAAGGGCTATGCCATTGGCCAGCGAGGATTGAACATGTCACTGAACCCAACCGCTACCA	117103
Qy	121	GGTGTTCCTTCTTCGGGACCCATGAGACCGCCCTGCTGGGCCCAAGCACCTTTTTCCTTA	180
Db	117104	GGTGTTCCTTCTTCGGGACCCATGAGACCGCCCTGCTGGGCCCAAGCACCTTTTTCCTTA	117163
Qy	181	TGAGGAGTCCAAGGAGAGGTTTCGGCAAGCCTAACAAAGAGGCGCGGCTTCAGTGAGGGGCT	240
Db	117164	TGAGGAGTCCAAGGAGAGGTTTCGGCAAGCCTAACAAAGAGGCGCGGCTTCAGTGAGGGGCT	117223
Qy	241	GTGGGAGATCGAGCACGACCCTATGGCTGAGGCCTCCCTTGCTGTGCCAGATGAGGA	300
Db	117224	GTGGGAGATCGAGCACGACCCTATGGTTGAGGCCTCCCTTGCTGTGCCAGATGAGGA	117283
Qy	301	GCAGCTTTGTGCCGAGGAGCCAGGGCCAGGAGAGGAGCCAGAGCCGGGGCAGGAGCTGGA	360
Db	117284	GCAGCTTTGTGCCGAGGAGCCAGGGCCAGGAGAGGAGCCAGAGCCGGGGCAGGAGCTGGA	117343
Qy	361	GCCGGAATCCAGGCCTGAGCTGGAATCCATGCCTGAGCTGGAGGCAGAACCAGAGGCCTGA	420
Db	117344	GCCGGAATCCAGGCCTGAGCTGGAATCCATGCCTGAGCTGGAGGCAGAACCAGAGGCCTGA	117403
Qy	421	GAAAGAGTGTGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCTGGAGCAGGAGCCGGA	480
Db	117404	GAAAGAGTGTGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCTGGA	117463
Qy	481	GCTGGAGCC-----GGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGAGCCCGA	534
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Qy	535	GCCGGAGCCGGAGCCCCAGCCTGCCTATGACCTACTGGATGCCAAGGAGGAGCCTGGCCT	594
Db	117524	GCCGGAGCCGGAGCCCCAGCCTGCCTATGACCTACTGGATGCCAAGGAGGAGCCTGGCCT	117583
Qy	595	CATTGAGGCCGAGCCAGGAGATCAGCAAGCCGAGCAAGTGCGAGAGCAGCACGCTGAAGC	654
Db	117584	CATTGAGGCCGAGCCAGGAGATCAGCAAGCCGAGCAAGTGCGAGAGCAGCACGCTGAAGC	117643
Qy	655	TGAGGTCATGGCTGTAGTGGAGGAGCCGGAGAGTCTGAAGAGGAGCGCGGAGGATGAACA	714
Db	117644	TGAGGTCATGGCTGTAGTGGAGGAGCCGGAGAGTCTGAAGAGGAGCGCGGAGGATGAACA	117703
Qy	715	GCCTCACAGTCCTCCCAAACGGCCAGGGAGGCGGCGCCTGGCGCGCTGGAGATGGAGCC	774
Db	117704	GCCTCACAGTCCTCCCAAACGGCCAGGGAGGCGGCGCCTGGCGCGCTGGAGATGGAGCC	117763
Qy	775	GGCTGGAGAGCGCGAGGCAGAGGCCTGCCCTTCGTGGAGGAGCCTGACCAAGCCCAGGA	834
Db	117764	GGCTGGAGAGCGCGAGGCAGAGGCCTGCCCTTCGTGGAGGAGCCTGACCAAGCCCAGGA	117823
Qy	835	ACAGCAGACTCCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTTGG	894
Db	117824	ACAGCAGACTCCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTTGG	117883
Qy	895	AGAAATCGAAGGCCTGTAGTCACGGTGTCTGTAAAAGAGCCCTCTCTACCCGTTCTGGT	954

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Qy 955 GCCACCTGGCTGTGGCTTGGGAAACCCGCTAGGGCC 990
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Db 117944 GCCACCTGGCTGTGGCTTGGGAAACCCGCTAGGGCC 117979

RESULT 3

AY061636

LOCUS AY061636 1512 bp mRNA linear ROD 13-NOV-2001
 DEFINITION Rattus norvegicus hepatoma-derived apoptotic-related protein mRNA,
 complete cds.

ACCESSION AY061636

VERSION AY061636.1 GI:16923254

KEYWORDS .

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 1512)

AUTHORS Tirado,O.M., Selva,D.M., Munell,F., Suarez-Quian,C. and Reventos,J.

TITLE A new member of the HDGF family, an apoptotic role?

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1512)

AUTHORS Tirado,O.M., Selva,D.M., Munell,F. and Reventos,J.

TITLE Direct Submission

JOURNAL Submitted (01-NOV-2001) URB, Hospitals Vall d'Hebron, Pso Vall
 d'Hebron 119-129, Barcelona, Spain

FEATURES Location/Qualifiers

source

1. .1512
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CDS

13. .903
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ORIGIN

Query Match 93.4%; Score 924.4; DB 6; Length 1512;
 Best Local Similarity 97.6%; Pred. No. 2.2e-213;
 Matches 966; Conservative 0; Mismatches 6; Indels 18; Gaps 2;

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Db 9 CGCTATGTCTTGCTTCAGCCGCCAAAATACAAGACCGGGGACCTGGTGTGTTGCCAAATT 68

Qy 61 AAAGGGCTATGCCCATTTGGCCAGCGAGGATTGAACATGTCACTGAACCCAACCGCTACCA 120
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Db 69 AAAGGGCTATGCCCATTTGGCCAGCGAGGATTGAACATGTCACTGAACCCAACCGCTACCA 128

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Db	129	GGTGTTCCTTCTTCGGGACCCATGAGACCGCCCTGCTGGGCCCCCAAGCACCTTTTTCCTTA	188
Qy	181	TGAGGAGTCCAAGGAGAGGTTTCGGCAAGCCTAACAAGAGGCGCGGCTTCAGTGAGGGGGCT	240
Db	189	TGAGGAGTCCAAGGAGAGGTTTCGGCAAGCCTAACAAGAGGCGCGGCTTCAGTGAGGGGGCT	248
Qy	241	GTGGGAGATCGAGCACGACCCTATGGCTGAGGCCTCCCTTGCCGTGTGCCCAGATGAGGA	300
Db	249	GTGGGAGATCGAGCACGACCCTATGGTTGAGGCCTCCCTTGCCGTGTGCCCAGATGAGGA	308
Qy	301	GCAGCTTTGTGCGGAGGAGCCAGGGCCAGGAGAGGAGCCAGAGCCGGGGCAGGAGCTGGA	360
Db	309	GCAGCTTTGTGCGGAGGAGCCAGGGCCAGGAGAGGAGCCAGAGCCGGGGCAGGAGCTGGA	368
Qy	361	GCCGGAATCCAGGCCTGAGCTGGAATCCATGCCTGAGCTGGAGGCAGAACCGAGGCCTGA	420
Db	369	GCCGGAATCCAGGCCTGAGCTGGAATCCATGCCTGAGCTGGAGGCAGAACCGAGGCCTGA	428
Qy	421	GAAAGAGTGTGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCTGGAGCAGGAGCCGGA	480
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Qy	481	GCTGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCCGAGCCGAGCCGGA	540
Db	489	GCAGGAGCCGGAGCTGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCCGAGCCGAGCCGGA	548
Qy	541	GCCGGAGCCCCAGCCTGCCTATGACCTACTGGATGCCAAGGAGGAGCCTGGCCTCATTGA	600
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Db	591	GGCCGAGCCAGGAGATCAGCAAGCCGAGCAAGTGCGAGAGCAGCACGCTGAAGCTGAGGT	650
Qy	661	CATGGCTGTAGTGGAGGAGCCGGAGAGTCTGAAGAGGAGCGCGGAGGATGAACAGCCTCA	720
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Qy	721	CAGTCCTCCCAAACGGCCAGGGAGGCGGCGCCTGGCGCGCTGGAGATGGAGCCGGCTGG	780
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Qy	781	AGAGCGCGAGGCAGAGGCCCTGCCCCTTCGTGGAGGAGCCTGACCAAGCCAGGAACAGCA	840
Db	771	AGAGCGCGAGGCAGAGGCCCTGCCCCTTCGTGGAGGAGCCTGACCAAGCCAGGAACAGCA	830
Qy	841	GACTCCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTTGGAGAAAT	900
Db	831	GACTCCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTTGGAGAAAT	890
Qy	901	CGAAGGCCTGTAGTCACGGTGTCTGTAAAAGAGCCCTCTCTACCCGTTCTGGTGCCACC	960
Db	891	CGAAGGCCTGTAGTCACGGTGTCTGTAAAAGAGCCCTCTCTACCCGTTCTGGTGCCACC	950
Qy	961	TGGCTGTGGCTTGGGAAACCCGCTAGGGCC	990
Db	951	TGGCTGTGGCTTGGGAAACCCGCTAGGGCC	980

RESULT 4

AF458587

LOCUS AF458587 909 bp mRNA linear PRI 10-JUN-2002

DEFINITION Homo sapiens hepatoma-derived growth factor HGDF5 mRNA, complete cds.

ACCESSION AF458587

VERSION AF458587.1 GI:21360801

KEY WORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 909)

AUTHORS Zhang, P.Z., Dong, Y.M., Shan, Y.X., Wei, Y.H., Guo, J.H. and Yu, L.

TITLE Direct Submission

JOURNAL Submitted (15-DEC-2001) School of Life Sciences, Institute of Genetics, Fudan University, Handan Road, 220, Shanghai 200433, China

FEATURES

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CDS

1. 909

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ORIGIN

Query Match 91.7%; Score 907.4; DB 5; Length 909;

Best Local Similarity 99.9%; Pred. No. 2.8e-209;

Matches 908; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 61 GGCTATGCCCATTTGGCCAGCGAGGATTGAACATGTCTACTGAACCCAAACCGTACCAGGTG 120

Qv 125 TTCTTCTTCGGGACCCATGAGACCGCCCTGCTGGGCCCCAAGCACCTTTTTCTTATGAG 184

Db 121 TTCTTCTTCGGGACCATGAGACCGCCCTGCTGGGCCCAAGCACCTTTTTCCTTATGAG 180

Ov 185 GAGTCCAAGGAGAGGTTCTGGCAAGCCTAACAAGAGGCGCGGCTTCAGTGAGGGGCTGTGG 244

Db 181 GAGTCCAAGGAGAGGGTTTCGGCAAGCCTAACAAGAGGCGCGGGCTTCAGTGAGGGGGCTGTGG 240

Ov 245 GAGATCGAGCACGACCCTATGGCTGAGGCCCTCCCCTTGCCTGTGCCCAGATGAGGAGCAG 304

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Db      301 CTTTGTGCCGAGGAGCCAGGGCCAGGAGAGGAGCCAGAGCCGGGGCAGGAGCTGGAGCCG 360
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Db      361 GAATCCAGGCCTGAGCTGGAATCCATGCCTGAGCTGGAGGCAGAACCGAGGCCTGAGAAA 420
Qy      425 GAGTGTGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCTGGAGCAGGAGCCGGAGCTG 484
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Db      421 GAGTGTGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCTGGAGCAGGAGCCGGAGCTG 480
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Qy      665 GCTGTAGTGGAGGAGCCGGAGAGTCTGAAGAGGAGCGCGGAGGATGAACAGCCTCACAGT 724
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RESULT 5

AF458586

LOCUS AF458586 921 bp mRNA linear ROD 24-JUL-2003

DEFINITION Rattus norvegicus hepatoma-derived growth factor variant, mRNA, complete cds.

ACCESSION AF458586

VERSION AF458586.1 GI:33187702

KEYWORDS

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 921)

AUTHORS Zhang,P.Z., Dong,Y.M., Shan,Y.X., Wei,Y.H., Guo,J.H. and Yu,L.
TITLE Direct Submission
JOURNAL Submitted (11-DEC-2001) School of Life Sciences, Intitute of
Genetics, Fudan University, Handan Road, 220, Shanghai 200433,
China

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FEATURES             Location/Qualifiers
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ORIGIN

Query Match 89.4%; Score 885.4; DB 6; Length 921;
Best Local Similarity 98.6%; Pred. No. 6.2e-204;
Matches 908; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

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Db	481	GAGCCGGAGCTGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCCGAGCCC	540
Qy	533	GAGCCGGAGCCGGAGCCCGAGCCTGCCTATGACCTACTGGATGCCAAGGAGGAGCCTGGC	592
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Qy	593	CTCATTGAGGCCGAGCCAGGAGATCAGCAAGCCGAGCAAGTGCGAGAGCAGCACGCTGAA	652
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Qy	653	GCTGAGGTCATGGCTGTAGTGGAGGAGCCGGAGAGTCTGAAGAGGAGCGCGGAGGATGAA	712
Db	661	GCTGAGGTCATGGCTGTAGTGGAGGAGCCGGAGAGTCTGAAGAGGAGCGCGGAGGATGAA	720
Qy	713	CAGCCTCACAGTCCTCCCAAACGGCCAGGGAGGCGGCGCCTGGCGCGCTGGAGATGGAG	772
Db	721	CAGCCTCACAGTCCTCCCAAACGGCCAGGGAGGCGGCGCCTGGCGCGCTGGAGATGGAG	780
Qy	773	CCGGCTGGAGAGCGCGAGGCAGAGGCCTGCCCTTCGTGGAGGAGCCTGACCAAGCCAG	832
Db	781	CCGGCTGGAGAGCGCGAGGCAGAGGCCTGCCCTTCGTGGAGGAGCCTGACCAAGCCAG	840
Qy	833	GAACAGCAGACTCCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTT	892
Db	841	GAACAGCAGACTCCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTT	900
Qy	893	GGAGAAATCGAAGGCCTGTAG	913
Db	901	GGAGAAATCGAAGGCCTGTAG	921

LOCUS (LOC): AF458587 GenBank (R)
 GenBank ACC. NO. (GBN): AF458587
 GenBank VERSION (VER): AF458587.1 GI:21360801
 CAS REGISTRY NO. (RN): 430805-71-3
 SEQUENCE LENGTH (SQL): 909
 MOLECULE TYPE (CI): mRNA; linear
 DIVISION CODE (CI): Primates
 DATE (DATE): 10 Jun 2002
 DEFINITION (DEF): Homo sapiens hepatoma-derived growth factor HGDF5 mRNA, complete cds.
 SOURCE: human.
 ORGANISM (ORGN): Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini;
 Hominidae; Homo
 NUCLEIC ACID COUNT (NA): 209 a 245 c 331 g 124 t
 REFERENCE: 1 (bases 1 to 909)
 AUTHOR (AU): Zhang,P.Z.; Dong,Y.M.; Shan,Y.X.; Wei,Y.H.; Guo,J.H.; Yu,L.
 TITLE (TI): Direct Submission
 JOURNAL (SO): Submitted (15-DEC-2001) School of Life Sciences,
 Institute of Genetics, Fudan University, Handan Road,
 220, Shanghai 200433, China

FEATURES (FEAT):

Feature Key	Location	Qualifier
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 13: geneseqn2004bs:*
 14: geneseqn2005s:*
 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	990	100.0	990	9	ADA37366	Ada37366 Human hep
2	885.4	89.4	921	11	ADQ96711	Adq96711 Human Wol
3	511.8	51.7	861	11	ADO59824	Ado59824 Human hep
4	505.2	51.0	882	2	AAV01730	Aav01730 Mouse liv
5	347.8	35.1	783	2	AAV57582	Aav57582 Nucleus-t
6	226.8	22.9	880	4	AAF30641	Aaf30641 Human hep
7	223.8	22.6	756	4	AAD16358	Aad16358 Human sbg

	8	223.8	22.6	794	12	ACH91708	Ach91708 Human gen
c	9	154	15.6	30191	12	ADQ97654	Adq97654 Mouse can
	10	148	14.9	2779	12	ADJ75971	Adj75971 Marker ge
	11	141.8	14.3	110000	14	ADZ12814_2	Continuation (3 of
	12	138.4	14.0	1744	15	AEF36279	Aef36279 Hepatoma-
c	13	138.4	14.0	247461	13	ABD33153	Abd33153 Murine ca
	14	137.8	13.9	714	2	AAT88420	Aat88420 Mouse hep
	15	137.8	13.9	1563	2	AAV03867	Aav03867 Mouse hep
	16	135	13.6	723	2	AAQ79903	Aaq79903 Human hep
	17	135	13.6	723	10	ADF10208	Adf10208 Human hep
	18	135	13.6	732	3	AAA40112	Aaa40112 Human HDG
	19	135	13.6	834	3	AAA40117	Aaa40117 Human HDG
	20	135	13.6	1386	5	AAF59292	Aaf59292 Human hHD
	21	135	13.6	2133	3	AAF18049	Aaf18049 Lung canc
	22	135	13.6	2219	12	ADQ83188	Adq83188 Human tum
	23	135	13.6	2219	12	ADQ84369	Adq84369 Human tum
	24	135	13.6	2219	13	ADQ85101	Adq85101 Human tum
	25	135	13.6	2219	13	ADQ83876	Adq83876 Human tum
	26	135	13.6	2219	13	ADQ86291	Adq86291 Human tum
	27	135	13.6	2219	13	ACN37480	Acn37480 Tumour-as
	28	135	13.6	2376	2	AAQ79902	Aaq79902 Human hep
	29	135	13.6	2376	3	AAA40118	Aaa40118 Human HDG
	30	135	13.6	2376	5	ABA83087	Aba83087 Hepatoma-
	31	135	13.6	2376	10	ADF10210	Adf10210 Human hep
	32	135	13.6	2376	10	ADK61214	Adk61214 Ovarian c
	33	135	13.6	2376	12	ADJ45234	Adj45234 Human hep
	34	135	13.6	2376	13	ADR25187	Adr25187 Breast ca
	35	135	13.6	2376	14	ADY14323	Ady14323 DNA encod
	36	135	13.6	2376	14	ADZ48952	Adz48952 Insulin s
	37	135	13.6	2376	15	AEE60970	Aee60970 Human pat
	38	135	13.6	2388	14	AED73424	Aed73424 Human pla
	39	133.4	13.5	2135	10	ADE31258	Ade31258 Human dia
	40	132	13.3	480	9	ACH45232	Ach45232 Human foe
	41	128.2	12.9	869	2	AAV39154	Aav39154 Lung grow
	42	127	12.8	1926	3	AAA50254	Aaa50254 Epstein B
	43	127	12.8	1926	4	AAF82902	Aaf82902 EBV tethe
	44	127	12.8	1926	10	ADK65580	Adk65580 Human her
	45	127	12.8	1926	14	ADV68155	Adv68155 Epstein-B

ALIGNMENTS

RESULT 1

ADA37366

ID ADA37366 standard; cDNA; 990 BP.

XX

AC ADA37366;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human hepatoma-derived growth factor 5 cDNA.

XX

KW ds; gene; cytostatic; antiinflammatory; gene therapy; human;

KW hepatoma-derived growth factor 5; HDGF5; diagnosis; malignant tumour;

KW surgical efficiency; liver cancer; hepatitis; inflammation.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 5..913

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FT          /*tag= a
FT          /product= "Human hepatoma-derived growth factor 5"
XX
PN WO2003057883-A1.
XX
PD 17-JUL-2003.
XX
PF 02-JAN-2003; 2003WO-CN000003.
XX
PR 11-JAN-2002; 2002CN-00110535.
XX
PA (YULL/) YU L.
XX
PI Yu L, Tang L, Guo Z, Zhang P, Dong Y;
XX
DR WPI; 2003-587131/55.
DR P-PSDB; ADA37367.
XX
PT Human hepatoma-derived growth factor 5 and encoded polynucleotide,
PT applicable in early diagnosis of malignant tumor, and development of
PT drugs for hepatitis and acute inflammatory in various organs.
XX
PS Claim 1; Page 10; 26pp; Chinese.
XX
CC The invention relates to an isolated DNA encoding a human hepatoma-
CC derived growth factor 5 (HDGF5), or sequences that have at least 70 %
CC homology to the HDGF5 sequence. The polynucleotide and its encoded
CC polypeptide are applicable in early diagnosis of malignant tumours,
CC monitoring surgical efficiency and prognosis of liver cancer, and
CC development of drugs for hepatitis and acute inflammation in various
CC organs. This sequence represents the human HDGF5 cDNA.
XX
SQ Sequence 990 BP; 221 A; 273 C; 354 G; 142 T; 0 U; 0 Other;

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Query Match 100.0%; Score 990; DB 9; Length 990;
Best Local Similarity 100.0%; Pred. No. 7.9e-176;
Matches 990; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	AAAGGGCTATGCCCATTTGGCCAGCGAGGATTGAACATGTCACTGAACCCAACCGCTACCA	120
Db	61	AAAGGGCTATGCCCATTTGGCCAGCGAGGATTGAACATGTCACTGAACCCAACCGCTACCA	120
Qy	121	GGTGTTCTTCTTCGGGACCCATGAGACCGCCCTGCTGGGCCCAAGCACCTTTTTCCTTA	180
Db	121	GGTGTTCTTCTTCGGGACCCATGAGACCGCCCTGCTGGGCCCAAGCACCTTTTTCCTTA	180
Qy	181	TGAGGAGTCCAAGGAGAGGTTCGGCAAGCCTAACAAGAGGC GCGCTTCAGTGAGGGGCT	240
Db	181	TGAGGAGTCCAAGGAGAGGTTCGGCAAGCCTAACAAGAGGC GCGCTTCAGTGAGGGGCT	240
Qy	241	GTGGGAGATCGAGCACGACCCTATGGCTGAGGCCTCCCCTTG CCTGTGCC CAGATGAGGA	300
Db	241	GTGGGAGATCGAGCACGACCCTATGGCTGAGGCCTCCCCTTG CCTGTGCC CAGATGAGGA	300
Qy	301	GCAGCTTTGTGCCGAGGAGCCAGGGCCAGGAGAGGAGCCAGAGCCGGGGCAGGAGCTGGA	360
Db	301	GCAGCTTTGTGCCGAGGAGCCAGGGCCAGGAGAGGAGCCAGAGCCGGGGCAGGAGCTGGA	360

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Qy      361  GCCGGAATCCAGGCCTGAGCTGGAATCCATGCCTGAGCTGGAGGCAGAACCGAGGCCTGA  420
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Db      361  GCCGGAATCCAGGCCTGAGCTGGAATCCATGCCTGAGCTGGAGGCAGAACCGAGGCCTGA  420

Qy      421  GAAAGAGTGTGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCTGGAGCAGGAGCCGGA  480
      |||
Db      421  GAAAGAGTGTGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCTGGAGCAGGAGCCGGA  480

Qy      481  GCTGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGA  540
      |||
Db      481  GCTGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGA  540

Qy      541  GCCGGAGCCCCAGCCTGCCTATGACCTACTGGATGCCAAGGAGGAGCCTGGCCTCATTGA  600
      |||
Db      541  GCCGGAGCCCCAGCCTGCCTATGACCTACTGGATGCCAAGGAGGAGCCTGGCCTCATTGA  600

Qy      601  GGCCGAGCCAGGAGATCAGCAAGCCGAGCAAGTGCAGAGAGCAGCACGCTGAAGCTGAGGT  660
      |||
Db      601  GGCCGAGCCAGGAGATCAGCAAGCCGAGCAAGTGCAGAGAGCAGCACGCTGAAGCTGAGGT  660

Qy      661  CATGGCTGTAGTGGAGGAGCCGGAGAGTCTGAAGAGGAGCGCGGAGGATGAACAGCCTCA  720
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Db      661  CATGGCTGTAGTGGAGGAGCCGGAGAGTCTGAAGAGGAGCGCGGAGGATGAACAGCCTCA  720

Qy      721  CAGTCCTCCCAAACGGCCAGGGAGGCGGCGCCTGGCGCGCTGGAGATGGAGCCGGCTGG  780
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Qy      781  AGAGCGCGAGGCAGAGGCCTGCCCCCTTCGTGGAGGAGCCTGACCAAGCCCAGGAACAGCA  840
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Db      781  AGAGCGCGAGGCAGAGGCCTGCCCCCTTCGTGGAGGAGCCTGACCAAGCCCAGGAACAGCA  840

Qy      841  GACTCCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTTGGAGAAAT  900
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Db      841  GACTCCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTTGGAGAAAT  900

Qy      901  CGAAGGCCTGTAGTCACGGTGTCTGTAAAAGAGCCCTCTCTACCCGTTCTGGTGCCACC  960
      |||
Db      901  CGAAGGCCTGTAGTCACGGTGTCTGTAAAAGAGCCCTCTCTACCCGTTCTGGTGCCACC  960

Qy      961  TGGCTGTGGCTTGGGAAACCCGCTAGGGCC  990
      |||
Db      961  TGGCTGTGGCTTGGGAAACCCGCTAGGGCC  990

```

RESULT 2

ADQ96711

ID ADQ96711 standard; cDNA; 921 BP.

XX

AC ADQ96711;

XX

DT 23-SEP-2004 (first entry)

XX

DE Human Wolf-Hirschhorn syndrome-related protein (WHSRP) cDNA.

XX

KW Wolf-Hirschhorn syndrome-related protein; WHSRP; cell differentiation;
development; human; ss; gene.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers
 FT CDS 1. .921
 FT /*tag= a
 FT /product= "Human Wolf-Hirschhorn syndrome-related protein
 FT (WHSRP)"
 XX
 PN CN1376796-A.
 XX
 PD 30-OCT-2002.
 XX
 PF 04-APR-2002; 2002CN-00111267.
 XX
 PR 04-APR-2002; 2002CN-00111267.
 XX
 PA (UYFU-) UNIV FUDAN.
 XX
 PI Yu L, Tang L, She X;
 XX
 DR WPI; 2003-202161/20.
 DR P-PSDB; ADQ96712.
 XX
 PT Coding sequence of novel human protein and its preparing process and
 PT application.
 XX
 PS Claim 1; SEQ ID NO 1; 17pp; Chinese.
 XX
 CC The invention relates to a novel cDNA sequence for the human Wolf-
 CC Hirschhorn syndrome-related protein (hWHSRP) which is associated with
 CC human cell differentiation and development and the encoded polypeptide,
 CC in addition to a process for preparing and applying the said
 CC polynucleotide and polypeptide sequences. The current sequence is that of
 CC the human WHSRP cDNA of the invention.
 XX
 SQ Sequence 921 BP; 212 A; 248 C; 337 G; 124 T; 0 U; 0 Other;

Query Match 89.4%; Score 885.4; DB 11; Length 921;
 Best Local Similarity 98.6%; Pred. No. 2.8e-156;
 Matches 908; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

Qy	5	ATGTCTTGCTTCAGCCGCCCAAAATACAAGACCGGGGACCTGGTGTGTTGCCAAATTAAAG	64
Db	1	ATGTCTTGCTTCAGCCGCCCAAAATACAAGACCGGGGACCTGGTGTGTTGCCAAATTAAAG	60
Qy	65	GGCTATGCCCATTGGCCAGCGAGGATTGAACATGTCACTGAACCCAACCGCTACCAGGTG	124
Db	61	GGCTATGCCCATTGGCCAGCGAGGATTGAACATGTCACTGAACCCAACCGCTACCAGGTG	120
Qy	125	TTCTTCTTCGGGACCCATGAGACCGCCCTGCTGGGCCCAAGCACCTTTTTCCTTATGAG	184
Db	121	TTCTTCTTCGGGACCCATGAGACCGCCCTGCTGGGCCCAAGCACCTTTTTCCTTATGAG	180
Qy	185	GAGTCCAAGGAGAGGTTCTGGCAAGCCTAACAGAGGCGCGGCTTCAGTGAGGGGCTGTGG	244
Db	181	GAGTCCAAGGAGAGGTTCTGGCAAGCCTAACAGAGGCGCGGCTTCAGTGAGGGGCTGTGG	240
Qy	245	GAGATCGAGCACGACCCTATGGCTGAGGCCTCCCCTTGCTGTGCCAGATGAGGAGCAG	304
Db	241	GAGATCGAGCACGACCCTATGGCTGAGGCCTCCCCTTGCTGTGCCAGATGAGGAGCAG	300
Qy	305	CTTTGTGCCGAGGAGCCAGGGCCAGGAGAGGAGCCAGAGCCGGGGCAGGAGCTGGAGCCG	364

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Db      301 CTTTGTGCCGAGGAGCCAGGGCCAGGAGAGGAGCCAGAGCCGGGGCAGGAGCTGGAGCCG 360
Qy      365 GAATCCAGGCCTGAGCTGGAATCCATGCCTGAGCTGGAGGCAGAACCGAGGCCTGAGAAA 424
      |||
Db      361 GAATCCAGGCCTGAGCTGGAATCCATGCCTGAGCTGGAGGCAGAACCGAGGCCTGAGAAA 420
Qy      425 GAGTGT-----GAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCTGGAGCAG 472
      |||
Db      421 GAGTGTGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCCGGAGCAGGAGCTGGAGCAG 480
Qy      473 GAGCCGGAGCTGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCC 532
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Db      481 GAGCCGGAGCTGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCGGAGCCC 540
Qy      533 GAGCCGGAGCCGGAGCCCCAGCCTGCCTATGACCTACTGGATGCCAAGGAGGAGCCTGGC 592
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Db      541 GAGCCGGAGCCGGAGCCCCAGCCTGCCTATGACCTACTGGATGCCAAGGAGGAGCCTGGC 600
Qy      593 CTCATTGAGGCCGAGCCAGGAGATCAGCAAGCCGAGCAAGTGCGAGAGCAGCACGCTGAA 652
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Db      601 CTCATTGAGGCCGAGCCAGGAGATCAGCAAGCCGAGCAAGTGCGAGAGCAGCACGCTGAA 660
Qy      653 GCTGAGGTCATGGCTGTAGTGGAGGAGCCGGAGAGTCTGAAGAGGAGCGCGGAGGATGAA 712
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Db      661 GCTGAGGTCATGGCTGTAGTGGAGGAGCCGGAGAGTCTGAAGAGGAGCGCGGAGGATGAA 720
Qy      713 CAGCCTCACAGTCCTCCCAAACGGCCCAGGGAGGCGGCGCCTGGCGCGCTGGAGATGGAG 772
      |||
Db      721 CAGCCTCACAGTCCTCCCAAACGGCCCAGGGAGGCGGCGCCTGGCGCGCTGGAGATGGAG 780
Qy      773 CCGGCTGGAGAGCGCGAGGCAGAGGCCTGCCCTTCGTGGAGGAGCCTGACCAAGCCCAG 832
      |||
Db      781 CCGGCTGGAGAGCGCGAGGCAGAGGCCTGCCCTTCGTGGAGGAGCCTGACCAAGCCCAG 840
Qy      833 GAACAGCAGACTCCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTT 892
      |||
Db      841 GAACAGCAGACTCCGTTGGAAGAAGAGGCCACAGAGGAGGCAGTCCAGGGCCTGATGGTT 900
Qy      893 GGAGAAATCGAAGGCCTGTAG 913
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Db      901 GGAGAAATCGAAGGCCTGTAG 921
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